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O I P E

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/884,948

DATE: 12/26/2001
 TIME: 16:19:42

Input Set : N:\CrF3\RULE60\09884948.raw
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1 <110> APPLICANT: YOKOYAMA, KEIICHI
 2 NAKAMURA, NAMI
 3 MIWA, TETSUYA
 4 SEGURA, KATSUYA
 5 <120> TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
 6 <130> FILE REFERENCE: 0010-0937-0
 7 <140> CURRENT APPLICATION NUMBER: 09/884,948
 8 <141> CURRENT FILING DATE: 2001-06-21
 9 <150> PRIOR APPLICATION NUMBER: 09/448,310
 10 <151> PRIOR FILING DATE: 1999-11-24
 11 <160> NUMBER OF SEQ ID NOS: 62
 12 <170> SOFTWARE: PatentIn Ver. 2.0
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 15 <211> LENGTH: 331
 16 <212> TYPE: PRT
 17 <213> ORGANISM: Artificial Sequence
 18 <220> FEATURE:
 19 <223> OTHER INFORMATION: Description of Artificial
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 25 20 25 30
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 27 35 40 45
 Lys Gln Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys
 28 50 55 60
 Val Gly Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu
 30 65 70 75 80
 Ala Phe Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn
 32 85 90 95
 Gly Arg Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val
 34 100 105 110
 Ala Lys Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu
 36 115 120 125
 Val Ala Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser
 38 130 135 140
 Ala Tyr Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala
 40 145 150 155 160
 Leu Arg Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn
 42 165 170 175
 Thr Pro Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg
 44 180 185 190
 Met Lys Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg
 46 195 200 205
 Ser Ser Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg

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52	Pro Arg Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr		240
53	245	250	255
54	Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp		
55	260	265	270
56	Thr His Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met		
57	275	280	285
58	His Val Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp		
59	290	295	300
60	Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn		
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77	1 5 10 15		
78	ccs gat cca tat cgt cca tct tat ggt cgt gct gaa act gtt gtt aat	96	
79	Pro Asp Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn		
80	20 25 30		
81	aat tat att cgt aaa tgg cca caa gtt tat tct cat cgt gat ggt cgt	144	
82	Asn Tyr Ile Arg Lys Trp Gln Val Tyr Ser His Arg Asp Gly Arg		
83	35 40 45		
84	aaa caa caa atg act gaa gaa caa cgt gaa tgg ctg tct tat ggt tgc	192	
85	Lys Gln Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys		
86	50 55 60		
87	gtt ggt gtt act tgg gtt aac tct ggt cag tat ccg act aac cgt ctg	240	
88	Val Gly Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu		
89	65 70 75 80		
90	gca ttc gct tcc ttc gat gaa gat cgt ttc aag aac gaa ctg aag aac	288	
91	Ala Phe Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn		
92	85 90 95		
93	ggt cgt ccg cgt tct ggt gaa act cgt gct gaa ttc gaa ggt cgt gtt	336	
94	Gly Arg Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val		
95	100 105 110		
96	gct aag gaa tcc ttc gat gaa gag aaa ggc ttc cag cgt gct cgt gaa	384	
97	Ala Lys Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu		
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99      gtt gct tct gtt atg aac cgt gct cta gag aac get cat gat gaa tct    432
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102     gct tac ctg gat aac ctg aag aag gaa ctg gct aac ggt aac gat gct    480
103     Ala Tyr Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala
104        145           150           155           160
105     ctg cgt aac gaa gat gct cgt tct tac tct gct ctg cgt aac    528
106     Leu Arg Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn
107        165           170           175
108     act ccg tcc ttc aaa gaa cgt aac ggt aac cat gat ccg tct cgt    576
109     Thr Pro Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg
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111     atg aaa gct gtt atc tac tct aaa cat ttc tgg tct ggt cag gat aga    624
112     Met Lys Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg
113        195           200           205
114     tct tct tct gct gat aaa cgt aaa tac ggt gat ccg gat gca ttc cgt    672
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117     ccg gct ccg ggt act ggt ctg gta gac atg tct cgt gat cgt aac atc    720
118     Pro Ala Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile
119        225           230           235           240
120     ccg cgt tct ccg act tct ccg ggt gaa ggc ttc gtt aac ttc gat tac    768
121     Pro Arg Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr
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123     ggt tgg ttc ggt gct cag act gaa gct gat gct gat aag act gta tgg    816
124     Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp
125        260           265           270
126     acc cat ggt aac cat tac cat gct ccg aac ggt tct ctg ggt gct atg    864
127     Thr His Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met
128        275           280           285
129     cat gta tac gaa tct aaa ttc cgt aac tgg tct gaa ggt tac tct gac    912
130     His Val Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp
131        290           295           300
132     ttc gat cgt ggt gct tac gtt atc acc ttc att ccg aaa tct tgg aac    960
133     Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn
134        305           310           315           320
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146 <222> LOCATION: (87)..(1082)
147 <400> SEQUENCE: 3
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150				Met	Asp	Ser	Asp	Asp	Arg	Val	Thr	Pro						
151				1					5									
152	cca	gct	gaa	cca	ctg	gat	cgt	atg	cca	tat	cgt	cca	tct	tat	161			
153	Pro	Ala	Glu	Pro	Leu	Asp	Arg	Met	Pro	Asp	Tyr	Arg	Pro	Ser	Tyr			
154	10			15				20			25							
155	ggt	cgt	gtc	gaa	act	gtt	aat	aat	tat	tat	cgt	aaa	tgg	caa	caa	209		
156	Gly	Arg	Ala	Glu	Thr	Val	Val	Asn	Asn	Tyr	Ile	Arg	Lys	Trp	Gln			
157				30				35			40							
158	gtt	tat	tct	cat	cgt	gat	ggc	gtt	aaa	cac	caa	atg	act	gaa	gaa	257		
159	Val	Tyr	Ser	His	Arg	Asp	Gly	Arg	Lys	Gln	Gln	Met	Thr	Glu	Gln			
160				45				50			55							
161	cgt	gaa	tgg	ctg	tct	tat	ggc	tgc	gtt	gtt	act	tgg	gtt	aac	tct	305		
162	Arg	Glu	Trp	Leu	Ser	Tyr	Gly	Cys	Val	Val	Thr	Trp	Val	Asn	Ser			
163				60				65			70							
164	ggc	cag	tat	ccg	act	aac	cgt	ctg	gca	tcc	gtc	tcc	gtt	gaa	gat	353		
165	Gly	Gln	Tyr	Pro	Thr	Asn	Arg	Leu	Ala	Phe	Ala	Ser	Phe	Asp	Glu	Asp		
166		75				80						85						
167	cgt	ttc	aag	aac	gaa	ctg	aag	aac	ggc	cgt	cgt	tct	tct	ggc	act	401		
168	Arg	Phe	Lys	Asn	Glu	Leu	Lys	Asn	Gly	Arg	Pro	Arg	Ser	Gly	Glu	Thr		
169		90			95				100			105						
170	cgt	gct	gaa	tcc	gaa	ggc	cgt	gtt	gtt	aaa	gtt	tcc	tcc	gtt	gaa	449		
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172		110			115				115			120						
173	aaa	ggc	tcc	cag	cgt	gtc	gaa	gtt	gtt	tct	gtt	atg	aac	cgt	gtc	497		
174	Lys	Gly	Phe	Gln	Arg	Ala	Arg	Glu	Val	Ala	Ser	Val	Met	Asn	Arg	Ala		
175		125			130				130			135						
176	cta	gag	aac	gct	cat	gat	gaa	tct	gtc	tac	ctg	gtt	aac	ctg	aag	545		
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178		140			145				145			150						
179	gaa	ctg	gct	aac	ggc	aat	gat	gtt	ctg	cgt	aat	gaa	gtt	gtt	cgt	593		
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181		155			160				160			165						
182	ccg	tcc	tac	tct	gtc	ctg	cgt	aat	act	ccg	tcc	tcc	aaa	gaa	cgt	641		
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184		170			175				180			185						
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186	Gly	Gly	Asn	His	Asp	Pro	Ser	Arg	Met	Lys	Ala	Val	Ile	Tyr	Ser	Lys		
187		190			195				195			200						
188	cat	tcc	tgc	tct	gtt	cag	gtt	aga	tct	tct	gtt	gtt	aaa	cgt	aaa	737		
189	His	Phe	Trp	Ser	Gly	Gln	Asp	Arg	Ser	Ser	Ala	Asp	Lys	Arg	Lys			
190		205			210				210			215						
191	tac	ggc	gtt	ccg	gat	gca	tcc	cgt	ccg	gtt	ggc	gtt	act	ggc	gtt	785		
192	Tyr	Gly	Asp	Pro	Asp	Ala	Phe	Arg	Pro	Ala	Pro	Gly	Thr	Gly	Leu	Val		
193		220			225				225			230						
194	gac	atg	tcc	tct	cgt	aat	atc	ccg	cgt	tct	ccg	gtt	act	tcc	ccg	833		
195	Asp	Met	Ser	Arg	Asp	Arg	Asn	Ile	Pro	Arg	Ser	Pro	Thr	Ser	Pro	Gly		
196		235			240				240			245						
197	gaa	ggc	tcc	gtt	aac	tcc	gtt	atc	ccg	gtt	tgg	tcc	ggc	gtt	cag	act	gaa	881

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205					285				290			295				
206	aac	tgg	tct	gaa	ggt	tac	tct	gac	ttc	gtt	cgt	ggt	gct	tac	gtt	atc
207	Asn	Trp	Ser	Glu	Gly	Tyr	Ser	Asp	Phe	Asp	Arg	Gly	Ala	Tyr	Val	Ile
208					300				305			310				
209	acc	tcc	att	ccg	aaa	tct	tgg	aac	act	gtt	ccg	gac	aaa	gtt	aaa	cag
210	Thr	Phe	Ile	Pro	Lys	Ser	Trp	Asn	Thr	Ala	Pro	Asp	Lys	Val	Lys	Gln
211					315				320			325				
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213	Gly	Trp	Pro													
214	330															
215	actaaaatag	acatatcta	tattatgt	gaa	ttttgt	gaca	tttccat	atag	gtt	gagg	gtt	gaa				
216	gg	tgatgt	at	aa	gtat	atgc	ccgg	atcg	catcg	ttgg	cc	ggc	atcac	ccg		
217	gcgc	acac	gg	tcgc	ttgt	gt	ggc	ccata	tcg	cc	acat	cac	cgat	gg	aa	gatcg
218	ctcg	ccact	cg	gg	gtc	atgc	gtt	tcg	gtt	gg	tt	at	gtt	gg	ca	
219	ccgg	gg	gg	at	tc	tc	tc	at	tc	cc	at	cc	t	tt	gg	gg
220	acgg	cc	tt	at	at	ct	at	gt	gt	tt	cc	at	at	gg	at	gg
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VERIFICATION SUMMARY

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